STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/553,906_

Source: _PCT_

Date Processed by STIC: _11/02/2005_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/553,906_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
                       prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
     Numbering   use **space characters**, instead.

4 ____ Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
                  ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
                       each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
                       residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
              previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
              the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
              Artificial or Unknown sequences.**

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for **each** skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                   This sequence is intentionally skipped

                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
     (NEW RULES)   <210> sequence id number
                   <400> sequence id number
                   000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                   In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
                 is Artificial Sequence

11 ____ Use of <220>   ~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~
                      Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                      "Unknown." Please explain source of genetic material in <220> to <223> section.
                      (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
               listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

```
RAW SEQUENCE LISTING              DATE: 11/02/2005
PATENT APPLICATION:  US/10/553,906   TIME: 09:45:22

       Input Set : A:\7175281710.txt
       Output Set: N:\CRF4\11022005\J553906.raw

   3 <110> APPLICANT: BERGMAN, Tomas
   4          DUAN, Rui-Dong
   5          NILSSON, Ake
   7 <120> TITLE OF INVENTION: Human Alkaline Sphingomyelinase and Use Thereof
   9 <130> FILE REFERENCE: 71752-81710
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/553,906
C--> 12 <141> CURRENT FILING DATE: 2005-10-21
  14 <160> NUMBER OF SEQ ID NOS: 18
  16 <170> SOFTWARE: PatentIn version 3.2
  18 <210> SEQ ID NO: 1
  19 <211> LENGTH: 458
  20 <212> TYPE: PRT
  21 <213> ORGANISM: Unknown
  23 <220> FEATURE:
  24 <223> OTHER INFORMATION: Unknown
  26 <400> SEQUENCE: 1
  28 Met Arg Gly Pro Ala Val Leu Leu Thr Val Ala Leu Ala Thr Leu Leu
  29 1               5                   10                  15
  32 Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
  33               20                  25                  30
  36 Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
  37           35                  40                  45
  40 Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
  41       50                  55                  60
  44 Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
  45 65                  70                  75                  80
  48 Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
  49                   85                  90                  95
  52 Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
  53               100                 105                 110
  56 Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
  57           115                 120                 125
  60 Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly
  61       130                 135                 140
  64 Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu
  65 145                 150                 155                 160
  68 Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile
  69               165                 170                 175
  72 Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr
  73               180                 185                 190
  76 Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu
  77           195                 200                 205
  80 Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly
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RAW SEQUENCE LISTING   DATE: 11/02/2005
PATENT APPLICATION: US/10/553,906   TIME: 09:45:22

Input Set : A:\7175281710.txt
Output Set: N:\CRF4\11022005\J553906.raw

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81     210                   215                   220
84 Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn
85 225                   230                   235                   240
88 Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala
89                   245                   250                   255
92 Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp
93                   260                   265                   270
96 Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro
97         275                   280                   285
100 Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His
101      290                   295                   300
104 Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His
105 305                   310                   315                   320
108 Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu
109                   325                   330                   335
112 Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu
113                   340                   345                   350
116 His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala
117         355                   360                   365
120 Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser
121      370                   375                   380
124 Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu
125 385                   390                   395                   400
128 Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr Glu
129                   405                   410                   415
132 Ser Ala Leu Pro Pro Asp Ala Leu Leu Val Ala Asp Gly Pro Cys Leu
133         420                   425                   430
136 Pro Ser Leu Ser Gln Ala Lys Gly Cys Met Pro Leu Ser Pro Ala Ala
137         435                   440                   445
140 Pro Thr Pro Ala Trp Leu Leu Trp Cys Trp
141      450                   455
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144 <210> SEQ ID NO: 2
145 <211> LENGTH: 1701
146 <212> TYPE: DNA
147 <213> ORGANISM: Unknown
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Unknown
152 <400> SEQUENCE: 2

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157 tcctggtgtc cttcgacggc ttccgctgga actacgacca ggacgtggac acccccaacc   180
159 tggacgccat ggcccgagac ggggtgaagg cacgctacat gacccccgcc tttgtcacca   240
161 tgaccagccc ctgccacttc accctggtca ccggcaaata tatcgagaac acggggtgg    300
163 ttcacaacat gtactacaac accaccagca aggtgaagct gccctaccac gccacgctgg   360
165 gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg   420
167 gcctgagggc tggctccttc ttctacccgg gcgggaacgt cacctaccaa ggggtggctg   480
169 tgacgcggag ccggaaagaa ggcatcgcac acaactacaa aaatgagacg gagtggagag   540
171 cgaacatcga cacagtgatg gcgtggttca cagaggagga cctggatctg gtcacactct   600
173 acttcgggga gccggactcc acgggccaca ggtacggccc cgagtccccg gagaggaggg   660
```

[handwritten annotations: "Same Error" with arrow pointing to line 150, and "Unknown" circled]

```
175 agatggtgcg gcaggtggac cggaccgtgg gctacctccg ggagagcatc gcgcgcaacc   720
177 acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca   780
179 aacgggctgg cgacctggtt gaattccaca agttccccaa cttcaccttc cgggacatcg   840
181 agtttgagct cctggactac ggaccaaacg ggatgctgct ccctaaagaa gggaggctgg   900
183 agaaggtgta cgatgccctc aaggacgccc accccaagct ccacgtctac aagaaggagg   960
185 cgttccccga ggccttccac tacgccaaca accccagggt cacacccctg ctgatgtaca  1020
187 gcgaccttgg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg  1080
189 gctttgacaa caaggacatg gacatgaaga ccatcttccg cgctgtgggc cctagcttca  1140
191 gggcgggcct ggaggtggag ccctttgaga gcgtccacgt gtacgagctc atgtgccggc  1200
193 tgctgggcat cgtgcccgag gccaacgatg ggcacctagc tactctgctg cccatgctgc  1260
195 acacagaatc tgctcttccg cctgatgctc tgctggtcgc ggacggaccc tgcctcccca  1320
197 gcttatccca ggccagaggc tgcatgccac tgtccccggc agcgccaacc cctgcttggc  1380
199 tgttatggtg ctggtaataa gcctgcagcc caggtccaaa gccccggcg agccggtccc  1440
201 ataaccggcc ccctgcccct gcccctgctc ctgctcctcc ccttcgggcc ccctcctcct  1500
203 gcaaaacccg ctcccgaagc ggcgctgccg tctgcagcca cgcgggggcg cgcgggagtc  1560
205 ttctgcgggc gctggaacct gcagacccgg cctcggtcag ctgggagggg cccgccccgg  1620
207 cacaaagcac ccatgggaat aaaggccaag ccgcgacagt cagcaaaaaa aaaaaaaaaa  1680
209 aaaaaaaaaa aaaaaaaaaa a                                            1701
212 <210> SEQ ID NO: 3
213 <211> LENGTH: 18
214 <212> TYPE: PRT
215 <213> ORGANISM: Unknown
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Unknown
220 <400> SEQUENCE: 3
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223 1               5                   10                  15
226 Lys Tyr
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231 <211> LENGTH: 458
232 <212> TYPE: PRT
233 <213> ORGANISM: Unknown
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Unknown
238 <400> SEQUENCE: 4
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241 1               5                   10                  15
244 Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
245             20                  25                  30
248 Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
249         35                  40                  45
252 Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
253     50                  55                  60
256 Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
257 65                  70                  75                  80
260 Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
261             85                  90                  95
264 Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
265             100                 105                 110
```

→ Same Error

→ Same Error

```
268 Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
269         115             120             125
272 Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly
273         130             135             140
276 Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu
277 145             150             155             160
280 Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile
281             165             170             175
284 Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr
285         180             185             190
288 Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu
289         195             200             205
292 Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly
293         210             215             220
296 Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn
297 225             230             235             240
300 Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala
301             245             250             255
304 Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp
305         260             265             270
308 Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro
309         275             280             285
312 Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His
313         290             295             300
316 Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His
317 305             310             315             320
320 Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu
321             325             330             335
324 Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu
325         340             345             350
328 His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala
329         355             360             365
332 Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser
333         370             375             380
336 Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu
337 385             390             395             400
340 Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr Glu
341             405             410             415
344 Ser Ala Leu Pro Pro Asp Gly Arg Pro Thr Leu Leu Pro Lys Gly Arg
345         420             425             430
348 Ser Ala Leu Pro Pro Ser Ser Arg Pro Leu Leu Val Met Gly Leu Leu
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353     450             455
356 <210> SEQ ID NO: 5
357 <211> LENGTH: 1878
358 <212> TYPE: DNA
359 <213> ORGANISM: Unknown
361 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 11/02/2005
PATENT APPLICATION: US/10/553,906   TIME: 09:45:22

Input Set : A:\7175281710.txt
Output Set: N:\CRF4\11022005\J553906.raw

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362 <223> OTHER INFORMATION: Unknown
365 <220> FEATURE:
366 <221> NAME/KEY: misc_feature
367 <222> LOCATION: (905)..(905)
368 <223> OTHER INFORMATION: n is a, c, g, or t
370 <400> SEQUENCE: 5
371 gtccatctgg aaggcccagc atgagaggcc cggccgtcct cctcactgtg gctctggcca      60
373 cgctcctggc tcccgggggcc ggagcaccgg tacaaagtca gggctcccag aacaagctgc     120
375 tcctggtgtc cttcgacggc ttccgctgga actacgacca ggacgtggac accccccaacc     180
377 tggacgccat ggcccgagac ggggtgaagg cacgctacat gaccccccgcc tttgtcacca     240
379 tgaccagccc ctgccacttc accctggtca ccggcaaata tatcgagaac cacggggtgg     300
381 ttcacaacat gtactacaac accaccagca aggtgaagct gccctaccac gccacgctgg     360
383 gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg     420
385 gcctgagggc tggctccttc ttctacccgg gcgggaacgt cacctaccaa ggggtggctg     480
387 tgacgcggag ccggaaagaa ggcatcgcac acaactacaa aaatgagacg gagtggagag     540
389 cgaacatcga cacagtgatg gcgtggttca cagaggagga cctggatctg gtcacactct     600
391 acttcggggga gccggactcc acgggccaca ggtacggccc cgagtccccg gagaggaggg     660
393 agatggtgcg gcaggtggac cggaccgtgg gctacctccg ggagagcatc gcgcgcaacc     720
395 acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca     780
397 aacgggctgg cgacctggtt gaattccaca agttccccaa cttcacccttc cgggacatcg     840
399 agtttgagct cctggactac ggaccaaacg ggatgctgct ccctaaagaa gggaggctgg     900
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W--> 401 **agaangtgta cgatgccctc aaggacgccc accccaagct ccacgtctac aagaaggagg**   960
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403 cgttccccga ggccttccac tacgccaaca accccagggt cacacccctg ctgatgtaca    1020
405 gcgaccttgg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg    1080
407 gctttgacaa caaggacatg gacatgaaga ccatcttccg cgctgtgggc cctagcttca    1140
409 gggcgggcct ggaggtggag ccctttgaga gcgtccacgt gtacgagctc atgtgccggc    1200
411 tgctgggcat cgtgcccgag gccaacgatg ggcacctagc tactctgctg cccatgctgc    1260
413 acacagaatc tgctcttccg cctgatggaa ggcctactct cctgcccaag ggaagatctg    1320
415 ctctcccgcc cagcagcagg cccctcctcg tgatgggact gctggggacc gtgattcttc    1380
417 tgtctgaggt cgcataacgc cccatggctc aaggaagccg ccgggagctg cccgcaggcc    1440
419 ctgggccggc tgtctcgctg cgatgctctg ctggtcgcgg acggaccctg cctcccccagc    1500
421 ttatcccagg ccagaggctg catgccactg tccccggcag cgccaacccc tgcttggctg    1560
423 ttatggtgct ggtaataagc ctcgcagccc aggtccagag cccccggcga gccggtccca    1620
425 taaccggccc cctgcccctg cccctgctcc tgctcctccc cttcgggccc cctcctcctg    1680
427 caaaacccgc tcccgaagcg gcgctgccgt ctgcagccac gcggggggcgc gcgggagctc    1740
429 tgcgggcgct ggaacctgca gacccggcct cggtcagctg ggaggggccc gccccggcac    1800
431 aaagcaccca tgggaataaa ggccaagccg cgacagtcag caaaaaaaaa aaaaaaaaaa    1860
433 aaaaaaaaaa aaaaaaaa                                                   1878
436 <210> SEQ ID NO: 6
437 <211> LENGTH: 415
438 <212> TYPE: PRT
439 <213> ORGANISM: Unknown
441 <220> FEATURE:
442 <223> OTHER INFORMATION: Unknown
444 <400> SEQUENCE: 6
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447 1               5                   10                  15
450 Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
451             20                  25                  30
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/02/2005
PATENT APPLICATION: US/10/553,906   TIME: 09:45:23

Input Set : A:\7175281710.txt
Output Set: N:\CRF4\11022005\J553906.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 905

VERIFICATION SUMMARY   DATE: 11/02/2005
PATENT APPLICATION: US/10/553,906   TIME: 09:45:23

Input Set : **A:\7175281710.txt**
Output Set: **N:\CRF4\11022005\J553906.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:900